

Run on:	March 17, 2003, 08:49:19	Search time 159 seconds (without alignments)	US-10-010-227-3	7	2055	50.7	695	27	US-60-360-039-9465	Sequence 9965, AP
Om protein - protein search, using sw model				8	2037.5	50.0	710	27	US-60-360-039-15849	Sequence 15849, AP
Copyright (c) 1993 - 2003 Compugen Ltd.				9	2018.5	49.8	711	27	US-60-360-039-15479	Sequence 15479, AP
Scoring table:	BLOSUM62			10	1995	49.2	752	27	US-60-360-039-94113	Sequence 9413, AP
Scanned:	Gapop 10.0 , Gapext 0.5			11	1978	48.8	755	27	US-60-360-039-7883	Sequence 7883, AP
Perfect score:	4055			12	1963.5	48.4	749	27	US-60-360-039-9308	Sequence 9308, AP
Sequence:	1 MPGAESTFQTLYDKVLQAHV..... KAVPVPTTNRGEEKKEPLEW	778		13	1955.5	48.2	681	27	US-60-360-039-8616	Sequence 8616, AP
Scoring table:	BLOSUM62			14	1891	46.6	740	27	US-60-360-039-7437	Sequence 7437, AP
Scanned:	Gapop 10.0 , Gapext 0.5			15	1881	46.4	729	27	US-60-360-039-4678	Sequence 4678, AP
Minimum DB seq length: 0				16	1861	45.9	686	27	US-60-360-039-7055	Sequence 7055, AP
Maximum DB seq length: 200000000				17	1857	45.8	688	27	US-60-360-039-4299	Sequence 4299, AP
Post-processing: Minimum Match 0%				18	1711.5	42.2	672	27	US-60-360-039-9059	Sequence 9059, AP
Database :	Pending Patents AA Main:*			19	1697.5	41.9	676	27	US-60-360-039-10463	Sequence 10463, A
	Listing first 100 summaries			20	1682.5	41.5	645	27	US-60-360-039-16463	Sequence 16643, A
				21	1670.5	41.2	679	27	US-60-360-039-14041	Sequence 14041, A
				22	1666.5	41.1	644	1	PCT-US02-03987-5730	Sequence 5730, AP
				23	1666.5	41.1	644	22	US-09-815-42-5730	Sequence 5730, AP
				24	1666.5	41.1	644	24	US-10-072-851-5730	Sequence 5730, AP
				25	1666.5	41.1	644	27	US-60-242-78-1009	Sequence 1009, AP
				26	1666.5	41.1	644	27	US-60-253-225-2535	Sequence 2353, AP
				27	1666.5	41.1	644	27	US-60-269-008-4336	Sequence 4336, AP
				28	1666.5	41.1	644	27	US-09-417-507-37934	Sequence 37934, AP
				29	1655.5	40.8	517	18	US-60-360-039-8819	Sequence 8819, AP
				30	1595.5	39.3	668	27	US-60-360-039-8819	Sequence 8819, AP
				31	1586	39.1	469	27	US-60-360-039-10002	Sequence 15002, A
				32	1555	38.3	469	24	US-10-015-227-10081	Sequence 10081, A
				33	1548.5	38.2	469	21	US-09-791-537-20546	Sequence 20646, A
				34	1545.5	38.1	469	21	US-09-791-537-33097	Sequence 33097, A
				35	1529.5	37.7	471	27	US-09-791-537-19706	Sequence 19706, A
				36	1520.5	37.5	526	17	US-09-328-3528-8024	Sequence 8024, AP
				37	1508	37.2	672	27	US-60-360-039-7323	Sequence 7323, AP
				38	1507.5	37.2	474	1	PCT-US02-03987-5127	Sequence 5127, AP
				39	1507.5	37.2	474	22	US-09-815-212-5127	Sequence 5127, AP
				40	1507.5	37.2	474	24	US-10-072-851-5127	Sequence 5127, AP
				41	1507.5	37.2	474	27	US-60-262-2683	Sequence 2683, AP
				42	1507.5	37.2	474	27	US-60-257-931-3511	Sequence 3511, AP
				43	1507.5	37.2	474	27	US-60-269-3108-4533	Sequence 4533, AP
				44	1507.5	37.2	480	16	US-60-269-3108-4533	Sequence 4533, AP
				45	1494	36.8	670	27	US-60-360-039-4565	Sequence 28668, A
				46	1483.5	36.6	466	21	US-09-791-537-15038	Sequence 15038, A
				47	1483.5	36.6	481	18	US-09-489-039-94-12322	Sequence 12322, A
				48	1481.5	36.5	466	21	US-09-791-537-2631	Sequence 2631, A
				49	1479.5	36.5	466	1	PCT-US02-03987-10021	Sequence 10021, A
				50	1479.5	36.5	466	21	US-09-791-537-2846	Sequence 2846, A
				51	1477.5	36.5	466	22	US-09-815-242-1021	Sequence 1021, A
				52	1479.5	36.5	466	24	US-10-012-851-10021	Sequence 10021, A
				53	1471	36.3	469	1	PCT-US01-03987-11164	Sequence 11164, A
				54	1471	36.3	469	21	US-09-791-537-84058	Sequence 84058, A
				55	1471	36.3	469	22	US-09-815-242-1164	Sequence 11164, A
				56	1471	36.3	469	24	US-09-815-242-1164	Sequence 11164, A
				57	1467.5	36.2	470	16	US-09-252-911-922	Sequence 9422, AP
				58	1467.5	36.2	470	16	US-09-252-6919C-9422	Sequence 9422, AP
				59	1450.5	35.8	466	1	PCT-US01-03987-14017	Sequence 14017, A
				60	1450.5	35.8	466	22	US-09-815-242-14017	Sequence 14017, A
				61	1450.5	35.8	466	24	US-10-012-851-14017	Sequence 14017, A
				62	1444.5	35.6	495	27	US-60-28-476-3203	Sequence 3203, AP
				63	1439.5	35.5	487	19	US-09-543-821A-7031	Sequence 7031, AP
				64	1432	35.3	465	21	US-09-791-537-84859	Sequence 84859, A
				65	1413	34.8	485	21	US-09-791-537-84859	Sequence 84859, A
				66	1399.5	34.5	475	21	US-09-791-537-10324	Sequence 10324, A
				67	1393.5	34.4	472	21	US-09-791-537-82623	Sequence 82623, A
				68	1385.5	34.2	473	21	US-09-791-537-80849	Sequence 80849, A
				69	1383.5	34.1	471	21	US-09-791-537-78936	Sequence 82611, A
				70	1383.5	34.0	466	21	US-09-791-537-74486	Sequence 74486, A
				71	1354.5	33.4	469	21	US-09-791-537-78936	Sequence 74486, A
				72	1354	33.4	476	21	US-09-791-537-78936	Sequence 74486, A
				73	1354	33.4	476	21	US-09-791-537-78936	Sequence 74486, A
				74	1347.5	33.2	481	21	US-09-738-626-4952	Sequence 4952, AP
				75	1330	32.8	471	21	US-09-791-537-50428	Sequence 50428, A
				76	1330	32.8	553	20	US-09-606-740A-266	Sequence 266, AP
				77	1321.5	32.6	384	21	US-09-449-11127	Sequence 11127, A
				78	1321.5	32.6	384	22	US-09-803-110-11127	Sequence 11127, A
				79	1316	32.5	384	22	US-09-606-740A-266	Sequence 266, AP

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	4055	100.0	778	US-10-010-0227-3
2	3397	83.8	840	US-10-0360-039-3233
3	2456.5	60.6	779	US-10-0360-039-21952
4	2451.5	60.5	794	US-10-179-131-8614
5	2076	51.2	644	US-09-791-537-121852
6	2068.5	51.0	875	US-60-360-039-7864
7	27			

RESULT 1  
US-10-010-227-3  
1 Sequence 3, Application US/10010227  
1 GENERAL INFORMATION:  
1 APPLICANT: Hauer, Lisbeth  
1 APPLICANT: Adachi, Kiichi  
1 APPLICANT: Dezaan, Todd M  
1 APPLICANT: Lo, Sze Chung C  
1 APPLICANT: Montenegro-Chamorro, Maria V  
1 APPLICANT: Frank, Sheryl A  
1 APPLICANT: Darveaux, Blaise A  
1 APPLICANT: Mahanty, Sanjaya K  
1 APPLICANT: Heiniger, Ryan W  
1 APPLICANT: Skalchunes, Amy R  
1 APPLICANT: Pan, Huagin  
1 APPLICANT: Tarpey, Rex  
1 APPLICANT: Shuster, Jeffrey R  
1 APPLICANT: Tanzer, Matthew M  
1 TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF INHIBITORS OF 3-ISOPROPYLMALATE  
1 TITLE OF INVENTION: DEHYDRATE AS ANTIBIOTICS  
1 FILE REFERENCE: 2131US  
1 CURRENT APPLICATION NUMBER: US/10/010 , 227  
1 CURRENT FILING DATE: 2001-12-06  
1 SOFTWARE: PatentIn version 3.1  
1 SEQ ID NO 3  
1 LENGTH: 778  
1 TYPE: PRT  
1 ORGANISM: Magnaporthe grisea

US-10-010-227-3

Query Match 100.0% ; Score 4055 ; DB 24 ; Length 778 ;  
Best Local Similarity 100.0% ; Pred. No. 0 ;  
Matches 778 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Qy 1 MPAQESTPQTLYDKVLOAHVYDEKLDTVLYIDRHLVHETSTSQAFLGLRNAGRKYRPP 60  
Db 1 MPAQESTPQTLYDKVLOAHVYDEKLDTVLYIDRHLVHETSTSQAFLGLRNAGRKYRPP 60

Qy 61 OCTLATTDHNVPTTSKALDIAF1KEDDSRTQCVTLEENKEFGVTVFGLSDKRQGIV 120  
Db 61 OCTLATTDHNVPTTSKALDIAF1KEDDSRTQCVTLEENKEFGVTVFGLSDKRQGIV 120

Qy 121 HVIGPSEQGFTLPGTTVUCGDSHTSSTGAFGAGTCTSEVHVLATQCLITKRSKNMRI 180  
Db 121 HVIGPSEQGFTLPGTTVUCGDSHTSSTGAFGAGTCTSEVHVLATQCLITKRSKNMRI 180

Sequence 55954, A  
Sequence 100996, A  
Sequence 90886, A  
Sequence 12156, A  
Sequence 12928, A  
Sequence 5398, A  
Sequence 6093, A  
Sequence 4865, A  
Sequence 15039, A  
Sequence 12928, A  
Sequence 12156, A  
Sequence 12928, A  
Sequence 10069, A  
Sequence 4865, A  
Sequence 19849, A  
Sequence 18971, A  
Sequence 81237, A  
Sequence 18414, A  
Sequence 131423, A  
Sequence 37932, A

Qy 181 QVDGEIAPGSSKDVLHAIGLIGTGGTGAIVFCCSVIRSLSPARMSTCNMSTEGGA 240  
Db 181 QVDGEIAPGSSKDVLHAIGLIGTGGTGAIVFCCSVIRSLSPARMSTCNMSTEGGA 240

Qy 241 RAGMYAPDEITPEYLKGRPLAKYDSDPGAKYDIDYFIDADIVP 300  
Db 241 RAGMYAPDEITPEYLKGRPLAKYDSDPGAKYDIDYFIDADIVP 300

Qy 301 TLTMGSPSPDVPTGVPDDETAPEAKADGRMLQYMGKAGTGFMDIPVDKVFTGS 360  
Db 301 TLTMGSPSPDVPTGVPDDETAPEAKADGRMLQYMGKAGTGFMDIPVDKVFTGS 360

Qy 361 CTNSR1EDRAAAVYKGKCKAPNTYSAMTYPGSGLVKTOAEEGDKIFEEAGFVREA 420  
Db 361 CTNSR1EDRAAAVYKGKCKAPNTYSAMTYPGSGLVKTOAEEGDKIFEEAGFVREA 420

Qy 421 GCSMCIGMNPDLAQOERCASTSNRNFEGROGAGGTHLMSPVMAAAAGIVGKLAIVRKL 480  
Db 421 GCSMCIGMNPDLAQOERCASTSNRNFEGROGAGGTHLMSPVMAAAAGIVGKLAIVRKL 480

Qy 481 TDYKSPHIAQKSTVTKPHDVERINQDAHEKDIIADIPDNNGHTNTSASVGTSAGL 540  
Db 481 TDYKSPHIAQKSTVTKPHDVERINQDAHEKDIIADIPDNNGHTNTSASVGTSAGL 540

ALIGNMENTS

RESULT 2  
US-10-360-039-3233  
1 Sequence 3233, Application US/60360039  
1 GENERAL INFORMATION:  
1 APPLICANT: Cao, Yongwei  
1 APPLICANT: Chen, Xianfeng  
1 APPLICANT: Goldman, Barry S  
1 APPLICANT: Hinkle, Gregory J  
1 APPLICANT: Slater, Steven C  
1 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
1 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
1 FILE REFERENCE: 38-10 (52052) A  
1 CURRENT APPLICATION NUMBER: US/60/360, 039  
1 CURRENT FILING DATE: 2002-02-21  
1 NUMBER OF SEQ ID NOS: 47374  
1 SEQ ID NO 3233  
1 LENGTH: 840  
1 TYPE: PRT  
1 ORGANISM: Neurospora crassa  
1 FEATURE: unsure  
1 LOCATION: (1) .. (840)  
1 OTHER INFORMATION: unsure at all Xaa locations

US-10-360-039-3233

Query Match 83.8% ; Score 3397 ; DB 27 ; Length 840 ;  
Best Local Similarity 77.8% ; Pred. No. 0 ;  
Matches 655 ; Conservative 53 ; Mismatches 60 ; Indels 74 ; Gaps 5 ;  
1 RTLYDKVLOAHVYDEKLDTVLYIDRHLVHETSTSQAFLGLRNAGRKYRPP 60

; SEQ ID NO 21952  
; LENGTH: 779  
; TYPE: PRT  
; ORGANISM: *Saccharomyces cerevisiae*  
; US-6-360-039-21952

Query Match 60.6%; Score 2456.5; DB 27; Length 779;  
Best Local Similarity 63.1%; Pred. No. 5.3e-236; Matches 486; Conservative 93; Mismatches 152; Indels 39; Gaps 10;  
Matches 486; Conservative 93; Mismatches 152; Indels 39; Gaps 10;  
Db 9 PRTLVYKVKFADAHVHODENGSPFLLYIDRHLVHEVTSPOAFEGLNAGRKVRPDCIATT 68  
Qy 8 PRTLVYKVKLQAIWVDEKLDGTWLYIDRHLVHEVTSPOAFEGLNAGRKVRPDCIATT 67  
Db 241 VQVGDGLAPGVSSKDVYLHVQIGPAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEAG 300  
Qy 240 ARAGWYAPDETFEYIKGRPLAPKYPNSPEWMIKATQWKRNLQSDPGAKYDIVFIDAKDIV 299  
Db 301 ARAGWYAPDETFEYIKGRPLAPKYPNSPEWMIKATQWKRNLQSDPGAKYDIVFIDAKDIV 360  
Qy 300 PTLTKGSPSPEDWVPTGWPUPPEFATEAKADGRMLQYQMLKAGTPMEDIPVDKVFIG 359  
Db 361 PTVTWGTSPEDWVPTGWPUPPEFATEAKADGRMLQYQMLKAGTPMEDIPVDKVFIG 420  
Qy 360 SCTNSRIEDLRAAVVUGRKKGKAPNVSAMVPGSGLVKTQAEEGLKDIFBEEAGFEMRE 419  
Db 421 SCTNSRIEDLRAAVVUGRKKGKLAANTIKRALITYPGSGLVKDREAEGLDKIFOEAGFEMRE 480  
Qy 420 AGCSMCIGMNPDLAFOERCASTSNRNFEGRCAGGTHLMSFVMAAAGIYVKGADWRK 479  
Db 481 AGCSMCIGMNPDLAFOERCASTSNRNFEGRCAGGTHLMSFVMAAAGIYVKGADWRK 540  
Qy 480 LTDYKSPHIAA--OKSTVTKPHVDERINDAHEKDITADIPEPDNGPHNTSASVG 536  
Db 541 LTDYKSPHIAA--OKSTVTKPHVDERINDAHEKDITADIPEPDNGPHNTSASVG 598  
Qy 537 SAGLKPKFTILKGIAAPLEKANVDTAIPKQFLKTIKETGLGNALFYEMRFNEDGETKSD 596  
Db 599 SAGLKPKFTILKGIAAPLEKANVDTAIPKQFLKTIKETGLGNALFYEMRFNEDGETKSD 658  
Qy 597 FVUNKEPKYRKAStLVCAGANFGCSSLREHAPWALNDIGIRSVIAPSADIPFNNFKGM 656  
Db 659 FVUNKEPKYRKAStLVCAGANFGCSSLREHAPWALNDIGIRSVIAPSADIPFNNFKGM 718  
Qy 657 LIPIKQDQOQIAAERAKGKEIIVDLPNQLKNTATCTCTIFEVERFRKVLNGDD 716  
Db 719 LIPIKQDQOQIAAERAKGKEIIVDLPNQLKNTATCTCTIFEVERFRKVLNGDD 778  
Qy 717 IGLTMQMDKIAFEAKMTRTPEWLGCTYLRKGQGQGLAAKAVPYTTNGEKEKPL 776  
Db 779 IGLTMQMDKIAFEAKMTRTPEWLGCTYLRKGQGQGLAAKAVPYTTNGEKEKPL 838  
Qy 777 EW 778  
Db 839 EW 840

RESULT 3  
US-60-039-21952  
; Sequence 21952, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slatner, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10 (52052)A  
; CURRENT APPLICATION NUMBER: US/60/160, 039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 473/4

RESULT 4  
US-10-179-131-8614  
; Sequence 8614, Application US/10179131  
; GENERAL INFORMATION:  
; APPLICANT: HARE, ROBERTA S.  
; APPLICANT: SHAW, KAREN J.  
; APPLICANT: SHIMER JR., GEORGE H.  
; APPLICANT: KESSLER, MARCO  
; APPLICANT: NOLLING, JORK  
; APPLICANT: ZENG, QIANDONG

CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES, CANDIDA ALBICANS						
APPLICANT:	GREENE, JONATHAN R.					
TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES, CANDIDA ALBICANS						
FILE REFERENCE:	2976-4031					
CURRENT APPLICATION NUMBER:	US/10/179,131					
CURRENT FILING DATE:	2002-06-21					
NUMBER OF SEQ ID NOS:	10194					
SEQ ID NO:	8614					
LENGTH:	794					
TYPE:	prt					
ORGANISM:	Candida albicans					
US-10-179-131-8614						
Query Match	60.5%	Score 2451.5;	DB 25;	Length 794;		
Best Local Similarity	61.6%	Pred. No. 1.8e-235				
Matches	90;	Mismatches 167;	Indels 49;	Gap 0		
Matches 491;	Conservative					
Qy	8	PQTYDKVLDQWVDEKLQDTVLLYIDRHLVHEVTSPOQAFEGLNAGKVRDRDCTLATT	6			
Db	21	PQTYDKVFDHVKKDSSSYLLYIDRHLVHEVTSPOQAFEGLNAGKRSVVRDCTLATT	8			
Qy	68	DHNPVPTTSRKALDITASPTKEDSSTQCVTLEENYKEFGVYTFGLSDKRGQIYVHVGPEQ	12			
Db	81	DHNPVPTTSRKANFKVNDSPFQEDDSRLLQVKTLLQVNKDFDVTYFQNTDDQGITHVVGPEQ	14			
Qy	128	GFTLPLGTTVYVGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELA	18			
Db	141	GFTLPLGTTVYVGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELA	20			
Qy	188	PGVSSKDVWVHLAIGLIGTAGGTGAVIEFCGSVNLSLHEARMSLCNSLEGGAGRMAT	24			
Db	201	EGTSKSDLVHLHVIGTAGGTGCVIEFGAKALENSLHEARMSLCNSMATEAGGRAGMCKP	26			
Qy	248	DEITPEYLKGRLPKPLAKYDSDPEWHRATQYKWRNLQSDPGAKYDIDVFDIDAKDIVPTLWTGTS	30			
Db	261	DEITPEYLKGRLPKP - SOEWKAMKWKLTIDEGAKDIDVFDIDKIASDIVPTLWTNS	31			
Qy	308	PEPYVPIGTVYVPDPETFAEKAKVADGRRMLQYMGKLKAGTPMEDIPIVDKVFIGSCTNSRIB	36			
Db	319	PQADLPIATSVDPVDPATVDPKISQGMRALKYQQLTPNTPFKEKIDKAFIGSCTNSRIB	37			
Qy	368	DLRAAAATVYKGKRAPIKAVNSAMVYPGSLGLVKTQAEERGLDKIIEEAGPEWREAGCSMLG	42			
Db	379	DLRAAAATVYKGKRAPIKAVNSAMVYPGSLGLVKTQAEERGLDKIIEEAGPEWREAGCSMLG	43			
Qy	428	MNPDLAPDPERCASTSNRNFEGRGGAGGRTHLMSPVMAAAAGIVGKFLADVRLKLTDYKASP	48			
Db	439	MNPDLAPDPERCASTSNRNFEGRGGAGGRTHLMSPVMAAAAGIVGKFLADVRLKLTDYKASP	49			
Qy	488	HIAAYQKSTVYKPH - VDEBRINQDA -- HEKDIADIPF ----- DNNQHPTNTSASV	53			
Db	494	-ATQDPEQIPIQAHEDKELQAVYEHEKEYEDTPQAEERLEDIPKDFEPFKRARTF	55			
Qy	535	-GTSAGIP -- KETILKGIAAPLEKANVDTAIIPKOFLKIKTRGLQNAFYERF-	58			
Db	552	IDNSAACGTSIDNSFKVLTGITYAPLYKANVDTAIIPKOFLKIKTRGKIKDFYELRFV	61			
Qy	588	-NEDGTE - KSDFTVLNEKPYRKASLLVCTGANFGCGSSREHAPWALNDFGIRSYTAPSFA	64			
Db	612	KGENGKDVETDPLVNTPEYKRAFLLVTDGNFEGCGSSREHAPWALKDFGIGKSTAPSFGD	67			
Qy	646	IEFNSFKNGMLPIPIKQQAQIAAAEARGKEIYDLPNQLIKATGET -- -ICTFE	70			
Db	672	IEFNSFKNGMLPIPIKQQAQIAAAEARGKEIYDLPNQLIKATGET -- -ICTFE	72			
Qy	702	VEFRKHLVINGDDIGTMQMDKIAFEAKNTRPFWLDTGTYLRRKGQQGKLAIAKAV	76			
Db	730	VEFRKHLVNGDDIGTMQMDKIAFEAKNTRPFWLDTGTYLRRKGQQGKLAIAKAV	77			
Qy	762	PVFTTNRGEKEKPLEW	778			
Db	778	PVFTTNRGEKEKPLEW	794			

RESULT 5	
US-09-791-537-121852	Sequence 121852, Application US/09791537
GENERAL INFORMATION:	
APPLICANT: Bionomix, Inc.	
APPLICANT: Debe, Derek	
APPLICANT: Danzer, Joseph	
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND METHODS OF USE THEREOF	
FILE REFERENCE: 261/210	
CURRENT APPLICATION NUMBER: US/09/791,537	
CURRENT FILING DATE: 2001-02-22	
NUMBER OF SEQ ID NOS: 15:055	
SOFTWARE: PatentIn version 3.0	
SEQ ID NO: 121852	
LENGTH: 644	
TYPE: PRT	
ORGANISM: <i>Mucor racemosus</i>	
US-09-791-537-121852	
Query Match 51.2%; Score 2076; DB 21; Length 644;	
Best Local Similarity 68.8%; Pred. No. 6e-18;	
Matches 407; Conservative 60; Mismatches 111; Indels 14; Gaps 6	
Qy 10 TLYDKVLOQAHVYDEKLQDGTVLILYDRLHLVTHEVTSQAAFFGLRNAGRKRVRPDCTLATTDH 69	
Db 51 TLYDKWQDDHVQDQEDTCCLAYDRLHLVTHEVTSQAAFFGLRNANRPRVRPDCTLATVDH 110	
Qy 70 NVPPTSRSKALKOJIASFIKEDDSRTQCTYLEENKEFGVTVYFGLSDKRGQVHVIGEQGF 129	
Db 111 NIPPTTTRKIFKNNTTFIKEADSRTOCTELEQNIKEAFLGTYFGMDSDRQGIVHVIGEQGF 170	
Qy 130 TLPGTTVCGDSHTSHTGAGLAFGIGSEVEHVLATCLITRSKNNMRIQVDGELAPG 189	
Db 171 TLPATTVCGDSHTSHTGAGLAFGIGSEVEHVLATQTLQKSKSKNNRKIRVQGKALPG 230	
Qy 190 VSSKDVVYLHAIGTIGTGTAGGTGAVIEFCGSVIRSLSMSMEAMSMICNSMIEGGARAGMVAPDE 249	
Db 231 VTSKDTVHLIIGTGTAGGTGCVIEFCGDTIAALSMESMSMICNSMIEGARAGMVAPDE 290	
Qy 250 ITFEYLGKRPLPKYDSPEWHKATQYKWNLQSDPGAKYIDYFIDAKD1VPTLTMGTSP 309	
Db 291 VTFEYLRDKPLAPK--GADWDRAVKYQNSLSSDAKYD1INVEINAADAPTLTMGTSPQ 348	
Qy 310 DVPVITGQVVPDPETFATEKKAQDGRRM1QYQMGKLAGTPMEDIYDVKVFIGSCTNSRIEDL 369	
Db 349 DVPVITGQVVPDPETFATEKKAQDGRRM1QYQMGKLAGTPMEDIYDVKVFIGSCTNSRIEDL 408	
Qy 370 RAAAAYVKGKKAQPNVSKAMAVYPGSGLVYKTOAEEGLDKIFEEAGEFEEWREAGCSMCLGMN 429	
Db 409 RAAAAYVKGKKAQPNVSKAMAVYPGSGLVYKTOAEEGLDKIFEEAGEFEEWREAGCSMCLGMN 467	
Qy 430 PDILAPOERCCASTSNRNFEGRGAGGRTILMSPVMAAAGIVGKLAQVKLTDYKASPHI 489	
Db 468 PDQLKGGERCASTSNRNFEGRGAGGRTILMSPVMAAAGIVGKLAQVKLTDYKASPHI 520	
Qy 490 AAYQKSTVTKPHDVERINQDAHEKD1IAD1IPDNNGPHNTSASVGTSGAGLPKETILKG1 549	
Db 521 SEIPGTPKQSPRQEYVAEEFSEDDB--DSSYVDSAP-VATPPBTGDSGMPKFTTKGY 577	
Qy 550 AAPPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRN-EDGTEKSDPVLN 600	

RESULT 6  
US-61-360-039-7864  
; Sequence 7864, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.  
 APPLICANT: Slater, Steven C.  
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 FILE REFERENCE: 38-10 (52052)A  
 CURRENT APPLICATION NUMBER: US/60/360, 039  
 CURRENT FILING DATE: 2002-02-21  
 NUMBER OF SEQ ID NOS: 47374  
 SEQ ID NO: 7864  
 LENGTH: 875  
 TYPE: PRT  
 ORGANISM: Rhodobacter sphaeroides  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (1)..(875)  
 OTHER INFORMATION: unsure at all Xaa locations  
 ; US-60-360-039-7864

Query Match 51.0%; Score 2068.5; DB 27; Length 875;

Best Local Similarity 49.1%; Pred. No. 5.9e-197; Mismatches 439; Conservative 95; Mismatches 184; Indels 177; Gaps 16;

Qy 4 ABSTPOTLYDKVULQAHVDEKLDTVILYIDRHLVHEUTSPQAFEGRLNAGRKRURPCT 63  
 Db 1 AMTAPRTLYDKWDDHHVHQSBGDTCLYIDRHLVHEUTSPQAFEGRLNAGRKRURPCT 60

Qy 64 LATTDHNVPTSRKALKDIAFSIKAEDDSRTQCVTLEENVKERQVYFGLSDKRQGIVHVI 123  
 Db 61 IAVPDHNVPTBGRDTK---IDNEBRSRIOVEALDKNARDFGINYVFSRDIQGIVHIV 115

Qy 124 GPEQGTPLGTRVWCDSDHTSPHARGCALAFIGTSVEFHVLATQCLITKRSKMRQYD 183  
 Db 116 GPEQGTPLGTMVCGSDHTATHGAGLAHGHTSEVEHVLATQCLITQKSKMRKVBT 175

Qy 184 GELAROVSXKOVULHAIGLIGTAGGTGAVIECGSVIRSLSMEARMSICNMSIEGARRAG 243  
 Db 176 GSLRGCVTAKOITLSQLGLTGTAGGTGCVIEYCGQAFELNSMEGRMTVNMAIEGARRAG 235

Qy 244 NVADPDETFEYKLKGRLPLAKYDSPEWHKATQWKNLQSDPGAKYDIDVFDIADKVIPVLT 303  
 Db 233 LIAPDESKTFAYVMGRPHPK- GAAWERALAYWKLTFDEGAQDFKVUTIRGEDIAPVVT 293

Qy 304 WGTSPSDVWVPTGQWVDPETATEAKKADGGRMLQYQMLKAGSTPMDIPVDKVPIGSCTN 363  
 Db 294 WGTSPSDVLPITATVPAEDF- TGGKVEAARRSLEYMQLTPGQKLTDPIDTVPIGSCTN 352

Qy 364 SRIEDJRAAAVVKGRKAKPNUKSAMVPGSGIWKTOQREBGLDKIFBAGFENWREAGCS 423  
 Db 353 GRIEDJRAAAETLKGKKAQGR- AMVTPGSGLVRQAEEEGLAQIFIDAGEFWRLAGCS 411

Qy 424 MCLGMNPDDILAPQBCASTSNRNPFGROGAGGRTHLMSPVMAAAGTVGKLADVRKLTDY 483  
 Db 412 MCLAMNPDDOLSPGERCASTSNRNPFGROGQRGRNTRHLVSPGMAAAAITGHLTDVRLMMA 471

Qy 484 KASP-----HIAVOKSTVKPHYDVERINDAHE-----KDIA-----D 518  
 Db 472 PAEPAXRPGQAQHSAPO-----VCSKGONGMKGKTSSSLVSGIALLGGTAALFP 523

Qy 519 IP-----EDNNGEHTNTSA----- 532

Db 524 LPVSLAVTVLACCVFVAVGAGFLWAARSSDRGKPSRGAAFFSPLVWVQWMLANPLAGM 583

Qy 533 -----SVGT-----SAGLPKTMILK----- 547

Db 584 VSITLMLGALFLVSGVVRIGLSSLATWRGTVMFMLMASSGLISAGLGLTILLRPEASJVL 643

Qy 548 -----GIAAPLEKANVDTDAIIPQF 568

Db 644 LGTLVAVELIVINGATLWANGFALKSGNPXAMQEFKTVTGVAAFPMLNIDTMIPQF 703

Qy 569 LTKTKRQGLGNALFYERFNEOCTEKSDPFLVNLKPYRCAISILVCTGANGFCGGSREHAPW 628  
 Db 704 LKTIQRSGLGKNLDFEMRYNPDCSEIPEPFVNLNPAYRDAOQIV-AGDNFGCGSSREHAPW 762

RESULT 7 US-60-039-9965  
 Sequence 9965, Application US/60360039  
 GENERAL INFORMATION:  
 APPLICANT: Cao, Yongwei  
 APPLICANT: Chen, Xinfeng  
 APPLICANT: Goldman, Barry S.  
 APPLICANT: Hinkle, Gregory J.  
 APPLICANT: Slater, Steven C.  
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 FILE REFERENCE: 38-10 (52052)A  
 CURRENT APPLICATION NUMBER: US/60/360, 039  
 CURRENT FILING DATE: 2002-02-21  
 NUMBER OF SEQ ID NOS: 47374  
 SEQ ID NO: 9965  
 LENGTH: 695

TYPE: PRT  
 ORGANISM: magnetite-containing magnetic coccus  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (1)..(695)  
 OTHER INFORMATION: unsure at all Xaa locations  
 ; US-60-039-9965

Query Match 50.7%; Score 2055; DB 27; Length 695;  
 Best Local Similarity 56.8%; Pred. No. 8.9e-196; Mismatches 422; Conservative 89; Mismatches 168; Indels 64; Gaps 11; Matches 422; Conservative 89; Mismatches 168; Indels 64; Gaps 11;

Qy 9 QTLKDVKULQAHVDEKLDTVILYIDRHLVHEUTSPQAFEGRLNAGRKRURPCTLATTD 68  
 Db 6 QTLFEKLNHLRITDEBGGSLIYDRLVHEUTSPQAFEGRLNAGRKRURPCTAVPD 65

Qy 69 HNVPTSRKALKDIAFSIKAEDDSRTQCVTLEENVKERQVYFGLSDKRQGIVHVI 128  
 Db 66 HNVPT-----KDLAGGIKOPVSKLQVDTIASNCQAFGIFTFGVSDLRQGVVHMAPEQ 119

Qy 129 FTLPGTTVVGDSHTSTHGFAGALAFGIGTSVEFHVLATQCLITKRSKMRQVNDGELAP 188  
 Db 120 ISLPGFTMVCDSDHTATHGAGLAHGHTSEVEHVLATQCLITQKSKMRQVNDGELPA 179

Qy 189 GVSKDVULHAIGLIGTAGGTGAVIECGSVIRSLSMEARMSICNMSIEGARRAGMAD 248  
 Db 180 GSTADQILITGNTGTTAGGTGCVIEBFGGSATQASMEGRMTVNMAIEGARRAGMAD 239

Qy 249 BTFEYKLKGRLPLAKYDSPEWHKATQWKNLQSDPGAKYDIDVFDIADKVIPVLTG 308  
 Db 240 EKTIAVQGRYPAKGEA- WEKAQAWQWQTKSDSAGPFDAVVTLARNIAFQVWTG 297

Qy 309 EDVVPITGVVWVDPETATEAKKADGGRMLQYQMLKAGSTPMDIPVDKVFIISCTNSRIED 368

Db 298 BLVAPVDPGVNPNTBPGNGKRGAMKALAVYMLQGRTGPMTEIAVUKVFIGSCTNSRIED 357

Qy 369 LRAAAVVKGRKAKPNUKSAMVNPESGLVQKTOAEBGLDKIFBAGFENWREAGCSMCLGM 428

Db 358 LRAAAVAVGKVKAAASIKLAVVPGTGLVKQQAEOGLDKIFWMEAGFEBWREPGCSMCLAM 417

Qy 429 NPDILAPQERCASSTSNRNPFGQRGAGGRTHLMSPVMAAAGTVGKLADVRKLTDXASPH 488  
 Db 418 NNDVLPGERCASTSNRNPFGROQDSRTHLVSPPMAMAAAAGHFVIR--NGKAS-G 473

Qy 489 IAAVOKSTVKPHYDVERINDAHEKDIADIPEDDNGPHTWTSASVGTSGAIPKFTLKG 548

Db	474	IAE-----VKXERTRPFMEA-----	Qy	549	IAPPLEKANVDTAIIPKQFLKTIKRTGLGNALFYEMRE-----NEDGTEKSDFV	Qy	549	IAPPLEKANVDTAIIPKQFLKTIKRTGLGNALFYEMRE-----NEDGTEKSDFV	Db	358	EDLRAAPAVAKRKVASTIKOALUVPPESGLVKAQAEERGLDKIFLDAFREWPGCSMCL	417
Qy	549	IAPPLEKANVDTAIIPKQFLKTIKRTGLGNALFYEMRE-----NEDGTEKSDFV	Db	496	IVAPLDRANVDTAIIPKQFLKTSKRSRGPNLFDDEWRYLQDGQPGKSNBGRPLNKDFV	555	IVAPLDRANVDTAIIPKQFLKTSKRSRGPNLFDDEWRYLQDGQPGKSNBGRPLNKDFV	Qy	427	GMNPDLIAQEQCASTSNRNFGRQGGRTHLMSPMAAGIVGKLAQDVKLTQDKAS	486	
Db	496	IVAPLDRANVDTAIIPKQFLKTSKRSRGPNLFDDEWRYLQDGQPGKSNBGRPLNKDFV	Qy	600	NKPYRKASILVCTGNGCSSREHAPWALNDEGIRSVIATPSADIFFNNSFKNGMLPI	659	NKPYRKASILVCTGNGCSSREHAPWALNDEGIRSVIATPSADIFFNNSFKNGMLPI	Db	418	AMNPDKLGSQHCASTSNRNFGRQGGRTHLMSPMAAGIVGKLAQDVKLTQDKAS	477	
Db	556	NKPYRAGARILLARD-NFGCGSSREHAPWALQDFGRVVIATPSADIFFNNSFKNGMLPI	614	NKPYRAGARILLARD-NFGCGSSREHAPWALQDFGRVVIATPSADIFFNNSFKNGMLPI	Db	478	PHIAAYOKSTVTPKHYDERINQDAHEKDIAIDIPEDINGPHTNTSASVGTSGASLKPFTIL	546				
Qy	660	PKDQQAQTEAIAAE- -AFAGKIEKEVDLDPNQLKNAUTGETCTTFFEEFRKHLVNGLDDI	717	PKDQQAQTEAIAAE- -AFAGKIEKEVDLDPNQLKNAUTGETCTTFFEEFRKHLVNGLDDI	Qy	487	PHIAAYOKSTVTPKHYDERINQDAHEKDIAIDIPEDINGPHTNTSASVGTSGASLKPFTIL	546				
Db	615	-VQEAQYDSLLEVAAPQGYTIVDLPDAQRITTPSGRSI-AFEVDPFRKHCLIHGLDDI	672	-VQEAQYDSLLEVAAPQGYTIVDLPDAQRITTPSGRSI-AFEVDPFRKHCLIHGLDDI	Db	478	E-XGIATSRUHPH-----HSLUPIPGIP-----MTPFTQH	507				
Qy	718	GTMQMDKIAPEAKMTRTPW	740	GTMQMDKIAPEAKMTRTPW	Qy	547	XGIAAPLEKANVDTAIIPKQFLKTIKRTGLGNALFYEMRE-----NEDGTEKS	597				
Db	673	GTLQHADQIAYESKHKQOPW	695	GTLQHADQIAYESKHKQOPW	Db	508	TGLVAPLDRANVDTDOIPKQFLKTSKRTGFGPNLFDWRYLDIGEGRDNSTRPLNQEF	567				
Qy	718	GTMQMDKIAPEAKMTRTPW	740	GTMQMDKIAPEAKMTRTPW	Qy	598	VLNKEPVRKASTLVCTQANFGCSSLRSHAPWALNDFGIRSVIATPSADLFPPNSFKNGML	657				
Db	673	GTLQHADQIAYESKHKQOPW	695	GTLQHADQIAYESKHKQOPW	Db	568	VINPFRYQASVILAR-ENFGCSSLRSHAPWALDEYGRAVIAPSADLFYNNFSFKNGML	626				
RESULT 8	US-60-360-039-154849	Sequence 15849, Application US/60360039	Qy	658	PIPIKODAQIEAAE- -ARAKIEYDLPNOLNIKNTGETCTFEEFRKHLVNGLDDI	715						
GENERAL INFORMATION:	Qy	658	PIPIKODAQIEAAE- -ARAKIEYDLPNOLNIKNTGETCTFEEFRKHLVNGLDDI	715								
APPLICANT: Cao, Yongwei	Db	627	PI-VLAEMDMLFBEQCLGNEGYQLTVDLAAQVRPDGVEY-AFEIDAFRKHCLUNGLD	684								
APPLICANT: Chen, Xianfeng	Qy	716	DIGLTMQMEDKIAPEAKMTRTPW	741								
APPLICANT: Goldman, Barry S.	Db	685	DIGLTMQDADALGRFEEQCHRAQOPW	710								
APPLICANT: Hinkle, Gregory J.	Qy	716	DIGLTMQDADALGRFEEQCHRAQOPW	710								
APPLICANT: Slater, Steven C.	Db	685	DIGLTMQDADALGRFEEQCHRAQOPW	710								
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES	RESULT 9	US-60-360-039-154779	Qy	716	DIGLTMQDADALGRFEEQCHRAQOPW	710						
FILE REFERENCE: 38-10(52052) A	Qy	716	DIGLTMQDADALGRFEEQCHRAQOPW	710								
CURRENT APPLICATION NUMBER: US/60/360,039	Db	627	PI-VLAEMDMLFBEQCLGNEGYQLTVDLAAQVRPDGVEY-AFEIDAFRKHCLUNGLD	684								
CURRENT FILING DATE: 2002-02-21	Qy	716	DIGLTMQMEDKIAPEAKMTRTPW	741								
NUMBER OF SEQ ID NOS: 47374	Db	685	DIGLTMQDADALGRFEEQCHRAQOPW	710								
SEQ ID NO 15849	Qy	716	DIGLTMQDADALGRFEEQCHRAQOPW	710								
TYPE: PRT	Db	685	DIGLTMQDADALGRFEEQCHRAQOPW	710								
ORGANISM: Xanthomonas campestris	Qy	716	DIGLTMQDADALGRFEEQCHRAQOPW	710								
FEATURE:	Db	685	DIGLTMQDADALGRFEEQCHRAQOPW	710								
NAME/KEY: unsure	Qy	716	DIGLTMQDADALGRFEEQCHRAQOPW	710								
LOCATION: (1) . (710)	Db	685	DIGLTMQDADALGRFEEQCHRAQOPW	710								
OTHER INFORMATION: unsure at all Xaa locations	Qy	716	DIGLTMQDADALGRFEEQCHRAQOPW	710								
US-60-360-039-15849	Db	685	DIGLTMQDADALGRFEEQCHRAQOPW	710								
Query Match	50.0%	Score 2027.5; DB 27; Length 710;	Qy	7	TPTOTLYDKVLAHIVDVKVDEKLDTVLYDIDHHLVHEVTSPQAEGIERNAGKVRVRPDCTLAT	66						
Best Local Similarity 50.4%	Pred. No. 5.3e-193; Mismatches 191; Indels 47; Gaps 11;	Db	1	TAKTLYDKLWHEVTRDDGSSIIYDIDHHLVHEVTSPQAEGIURLAGRKPWRDANIA	60							
Matches 421; Conservative	Qy	7	TDHNVPTTSRKALKDIAFIKEEDDSRTOCVTLEENVKPFTYFGLSDKRGQYHVIGPE	126								
FEATURE:	Db	61	TDHNVPTTSRKALKDIAFIKEEDDSRTOCVTLEENVKPFTYFGLSDKRGQYHVIGPE	119								
NAME/KEY: unsure	Qy	7	QFTLPLGTTVCGDSHTSTHGAGALATGIGTSEVHATQCLITKRSKMRQYDQGEL	186								
LOCATION: (1) . (710)	Db	120	QGATLPGMTVCGDSHTSTHGAGALATQCLJAKKMKMOMVRVEGTL	179								
OTHER INFORMATION: unsure at all Xaa locations	Qy	7	QGATLPGMTVCGDSHTSTHGAGALATGIGTSEVHATQCLITKRSKMRQYDQGEL	186								
US-60-360-039-15849	Db	120	QGATLPGMTVCGDSHTSTHGAGALATQCLJAKKMKMOMVRVEGTL	179								
Query Match	50.0%	Score 2027.5; DB 27; Length 710;	Qy	187	APCVSSKDVLIHALIGIIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	246						
Best Local Similarity 50.4%	Pred. No. 5.3e-193; Mismatches 191; Indels 47; Gaps 11;	Db	180	APCVSSKDVLIHALIGIIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	239							
Matches 421; Conservative	Qy	187	APCVSSKDVLIHALIGIIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	246								
FEATURE:	Db	180	APCVSSKDVLIHALIGIIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	239								
NAME/KEY: unsure	Qy	187	APCVSSKDVLIHALIGIIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	246								
LOCATION: (1) . (710)	Db	180	APCVSSKDVLIHALIGIIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	239								
OTHER INFORMATION: unsure at all Xaa locations	Qy	187	APCVSSKDVLIHALIGIIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	246								
US-60-360-039-15849	Db	180	APCVSSKDVLIHALIGIIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	239								
Query Match	50.0%	Score 2027.5; DB 27; Length 710;	Qy	247	PDEITFEYIKGPIAKYDPSPEWHKATQWKNLQSDPGAKYDIDVFTIDKIVPTLTWGT	306						
Best Local Similarity 50.4%	Pred. No. 5.3e-193; Mismatches 191; Indels 47; Gaps 11;	Db	240	VDKTKTIAVKGRIFAPK-GAIDAAVALWRLTVSDADASFTVVELRAEDIKQVSWGT	297							
Matches 421; Conservative	Qy	247	PDEITFEYIKGPIAKYDPSPEWHKATQWKNLQSDPGAKYDIDVFTIDKIVPTLTWGT	306								
FEATURE:	Db	240	VDKTKTIAVKGRIFAPK-GAIDAAVALWRLTVSDADASFTVVELRAEDIKQVSWGT	297								
NAME/KEY: unsure	Qy	247	PDEITFEYIKGPIAKYDPSPEWHKATQWKNLQSDPGAKYDIDVFTIDKIVPTLTWGT	306								
LOCATION: (1) . (710)	Db	240	VDKTKTIAVKGRIFAPK-GAIDAAVALWRLTVSDADASFTVVELRAEDIKQVSWGT	297								
OTHER INFORMATION: unsure at all Xaa locations	Qy	247	PDEITFEYIKGPIAKYDPSPEWHKATQWKNLQSDPGAKYDIDVFTIDKIVPTLTWGT	306								
US-60-360-039-15849	Db	240	VDKTKTIAVKGRIFAPK-GAIDAAVALWRLTVSDADASFTVVELRAEDIKQVSWGT	297								
Query Match	49.8%	Score 2018.5; DB 27; Length 711;	Qy	9	QFLYDQVLUQAHVVDKEUDKGTVLXLYDHLVHEVTSPQAEGIERNAGKVRVRPDCTLAT	68						
Best Local Similarity 56.1%	Pred. No. 4.3e-192; Mismatches 192; Indels 49; Gaps 1	Db	2	KTLYDQWEMHETTRDDGSSIIYDIDHHLVHEVTSPQAEGIERNAGKVRVRPDCTLAT	61							
Matches 419; Conservative	Qy	9	QFLYDQVLUQAHVVDKEUDKGTVLXLYDHLVHEVTSPQAEGIERNAGKVRVRPDCTLAT	68								
FEATURE:	Db	2	KTLYDQWEMHETTRDDGSSIIYDIDHHLVHEVTSPQAEGIERNAGKVRVRPDCTLAT	61								
NAME/KEY: unsure	Qy	9	QFLYDQVLUQAHVVDKEUDKGTVLXLYDHLVHEVTSPQAEGIERNAGKVRVRPDCTLAT	68								
LOCATION: (1) . (711)	Db	2	KTLYDQWEMHETTRDDGSSIIYDIDHHLVHEVTSPQAEGIERNAGKVRVRPDCTLAT	61								
OTHER INFORMATION: unsure at all Xaa locations	Qy	9	QFLYDQVLUQAHVVDKEUDKGTVLXLYDHLVHEVTSPQAEGIERNAGKVRVRPDCTLAT	68								
US-60-360-039-15479	Db	2	KTLYDQWEMHETTRDDGSSIIYDIDHHLVHEVTSPQAEGIERNAGKVRVRPDCTLAT	61								
Query Match	49.8%	Score 2018.5; DB 27; Length 711;	Qy	129	FTLPGTTVCGDSHTSTHGAGALATQCLITKRSKMRQYDQGEL	188						
Best Local Similarity 56.1%	Pred. No. 4.3e-192; Mismatches 192; Indels 49; Gaps 1	Db	121	ATLPGMTVCGBSHTSTHGAGALAHGTTSEYHVAQCLAKKMQNQVREVGTLPP	180							
Matches 419; Conservative	Qy	129	FTLPGTTVCGDSHTSTHGAGALATQCLITKRSKMRQYDQGEL	188								
FEATURE:	Db	121	ATLPGMTVCGBSHTSTHGAGALAHGTTSEYHVAQCLAKKMQNQVREVGTLPP	180								
NAME/KEY: unsure	Qy	129	FTLPGTTVCGDSHTSTHGAGALATQCLITKRSKMRQYDQGEL	188								
LOCATION: (1) . (711)	Db	121	ATLPGMTVCGBSHTSTHGAGALAHGTTSEYHVAQCLAKKMQNQVREVGTLPP	180								
OTHER INFORMATION: unsure at all Xaa locations	Qy	129	FTLPGTTVCGDSHTSTHGAGALATQCLITKRSKMRQYDQGEL	188								
US-60-360-039-15479	Db	121	ATLPGMTVCGBSHTSTHGAGALAHGTTSEYHVAQCLAKKMQNQVREVGTLPP	180								
Query Match	49.8%	Score 2018.5; DB 27; Length 711;	Qy	69	HNVPTRTSRKALKDIAFIKEEDDSRTOCVTLEENVKPFTYFGLSDKRGQVHYVGEQ	128						
Best Local Similarity 56.1%	Pred. No. 4.3e-192; Mismatches 192; Indels 49; Gaps 1	Db	62	HNVPTRTAERQGLS-ISDETSRLOQTLDECDGFLGEEQRGKWRIDANITPD	120							
Matches 419; Conservative	Qy	69	HNVPTRTSRKALKDIAFIKEEDDSRTOCVTLEENVKPFTYFGLSDKRGQVHYVGEQ	128								
FEATURE:	Db	62	HNVPTRTAERQGLS-ISDETSRLOQTLDECDGFLGEEQRGKWRIDANITPD	120								
NAME/KEY: unsure	Qy	69	HNVPTRTSRKALKDIAFIKEEDDSRTOCVTLEENVKPFTYFGLSDKRGQVHYVGEQ	128								
LOCATION: (1) . (711)	Db	62	HNVPTRTAERQGLS-ISDETSRLOQTLDECDGFLGEEQRGKWRIDANITPD	120								
OTHER INFORMATION: unsure at all Xaa locations	Qy	69	HNVPTRTSRKALKDIAFIKEEDDSRTOCVTLEENVKPFTYFGLSDKRGQVHYVGEQ	128								
US-60-360-039-15479	Db	62	HNVPTRTAERQGLS-ISDETSRLOQTLDECDGFLGEEQRGKWRIDANITPD	120								
Query Match	49.8%	Score 2018.5; DB 27; Length 711;	Qy	189	GVSSKDVVLHAIGIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	248						
Best Local Similarity 56.1%	Pred. No. 4.3e-192; Mismatches 192; Indels 49; Gaps 1	Db	181	GVTAKDVLAVIGKIGTAGGCHALEPAGSA-TRALNSERGMTCNMSIEAGARVAVD	240							
Matches 419; Conservative	Qy	189	GVSSKDVVLHAIGIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	248								
FEATURE:	Db	181	GVTAKDVLAVIGKIGTAGGCHALEPAGSA-TRALNSERGMTCNMSIEAGARVAVD	240								
NAME/KEY: unsure	Qy	189	GVSSKDVVLHAIGIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	248								
LOCATION: (1) . (711)	Db	181	GVSSKDVVLHAIGIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	248								
OTHER INFORMATION: unsure at all Xaa locations	Qy	189	GVSSKDVVLHAIGIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	248								
US-60-360-039-15479	Db	181	GVSSKDVVLHAIGIIGTAGGTGAVIEPGSVIRSLSMEARMSCTNMSTEGGARAGMVA	248								









RESULT 17  
 US-60-360-039-4299  
 ; Sequence 4299, Application US/60360039  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Chen, Xianfeng  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-101520521A  
 ; CURRENT APPLICATION NUMBER: US/60/360,039  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO: 4299  
 ; LENGTH: 688  
 ; TYPE: PRT  
 ; ORGANISM: Burkholderia fungorum  
 ; US-60-360-039-4299

Query Match 45.8%; Score 1857; DB 27; Length 688;  
 Best Local Similarity 51.3%; Pred. No. 6.6e-176; Mismatches 189; Indels 86; Gaps 10;  
 Matches 386; Conservative 92; MisMatches 189; Indels 86; Gaps 10;

QY 6 STPQTYLKVQVQAHVDEKLDGTUVTYDRLHVHEVTSPQATEGLRNAGRKVRRPDCTLA 65  
 Db 5 TSPRTLKLWOSHVAETPNTGPTLIVDRHLVIEVTSPQAERLUSGRKWRPPEVLA 64

QY 66 TTDHNHPT----TSLKALKDASFIKEEDDSRTQCVCVILEENKEFGTYFGSDKQGIV 120  
 Db 65 VADHNVPTIAERTSMDAIDPL----SRIQAOGLDKNCKFGIKSYGIRNPOOGII 117

QY 121 HVIGPECGTFLPGTVCGDSHTSTHGARGALAFGIGTSEVERVHLATOCCLITRKSKRMRI 180  
 Db 118 HVIGPELGATLPGMTVQAGDSHTSTHGAAALAFGVTSEVERVHLATOCCLSTYQKMSMLV 177

QY 181 QVGDGEALPGVSSKDVKVRAIGITGAGTGTGAVIEFCGSVIRSLSMEARMSICNMSLGGGA 240  
 Db 178 NVEGVLPVGVTAKVLLIRRTGTTAGGTGYAMEFAGSSTIRLSEMEGRNLICMNAIEAGA 237

QY 241 RAGMVADEDETEYKLKRPPLAKYDSEPHWKATOQWKLQSLSPGAKYDIDVFDKDV 300  
 Db 238 RVGLGIVDVTIDYVKGPFAFA-EAHWDAAVAYWRITLVSADARFDKIVNIDATORLP 295

QY 301 TLTWGSPPBDVPIGTVWDPDTFATEAKKANGRMQYMGKAGTPEMDIVDKVFIGS 360  
 Db 296 MYTWGTSBEMVUTDAPPNPLDPPVRATMAGALTYMGLPPTSLKSISLDKLFIGS 355

QY 361 CTNSRIBEDRLLAAVVKGRKKAQPKVNSAANVPGSGLYVQIAQEEBGLDKLFEEAGFENREA 420  
 Db 356 CTNARIELDRAAAVVKGRHVAFTVQALWVPGSGLYVQAAEGLDAAKPEAGFEEREP 415

QY 421 GCSMCLGNPDILAPOERCASTSNRNPBGRQGAGGRTHLSPVMAAGIVGKLADYRKL 480

RESULT 18  
 US-60-360-039-9059  
 ; Sequence 9059, Application US/60360039  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Chen, Xianfeng  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-101520521A  
 ; CURRENT APPLICATION NUMBER: US/60/360,039  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO: 9059  
 ; LENGTH: 672  
 ; TYPE: PRT  
 ; ORGANISM: Chloroflexus aurantiacus  
 ; US-60-360-039-9059

Query Match 42.2%; Score 1711.5; DB 27; Length 672;  
 Best Local Similarity 49.2%; Pred. No. 2.6e-161; Mismatches 210; Indels 63; Gaps 12;  
 Matches 358; Conservative 97; MisMatches 210; Indels 63; Gaps 12;

QY 8 PQTQYKVLQAHV--DEKLDGTUVTYDRLHVHEVTSPQATEGLRNAGRKVRRPDCTLAT 66  
 Db 1 PRTEFKEWHLVRPETAETPAVLYIDLHLTHEVTSPQAERLUSGRKWRPPEVLA 60

QY 67 TDHNVPTTSRKALKDASFIKEEDDSRTQCVCVILEENKEFGTYFGSDKQGIVHVIGE 126  
 Db 61 MDHSTPTPRNHLGIP--VDPMAISQLEQSLRCKNCAEGFPLFELGDENGQIVHVIGE 118

QY 127 QSPTRGTTVWCGDSHTSTHGARGALAFGIGTSEVERVHLATOCCLITRKSKRMRI 186  
 Db 119 QGJITQPGMTIVEGDSHTSTHGARGALAFGIGTSEVERVHLATOCCLQKPKTCAVRIGRL 178

QY 187 ACQVSSKDVKVRAIGITGAGTGTGAVIEFCGSVIRSLSMEARMSICNMSLGGGA 246  
 Db 179 GPTVAKDITLAKIYKVGGGTVYFEYMGAIRALSMEERMTCNMSIEGGRAGNA 238

QY 247 PDEITPEYLKGPLAKYDSEPHWKATOQWKLQSLSPGAKYDIDVFDKDV 306  
 Db 239 PDDTTEYVLAGPFAFA-GADEFAAARWRTRLPSDGAETDHELTLSASELKPMITYGT 296

QY 307 SPEDVWVPTGTVWDPDTFATEAKKANGRMQYMGKAGTPEMDIVDKVFIGSCTNSRI 366  
 Db 297 NPGMGIPIADPPRDPMDPDRSRAALDKALYMLGPGKPLIHPDVFIGSCTNSRL 356

367 EDJRAAAAVVKGRKKAPVKSAMVPGSGLVKTQAEEGLDK1FEEAGFEWRAAGCSMCL 426  
 Qy 249 EITFEWLKGRPLAPKVDSPWVKATQYWKNUQSDPQAKYDLDVFIADKDIVPTLNGTSP 308  
 Db 357 SDLRQAQCFERGRKVAPSVR - VMVPGSQQVKRKEAAEGLDRIFKEAGEWREAGCSACL 415  
 Db 235 ETTEFYIKGREFAPK - GAKWDEAVYWKTLYSDDSAVEDKTLKYDAADIGMITYGTNP 292  
 Qy 427 GMNPDLAQPQERCASTSNRNFEGROGAQGRTHIMSPYNAAGIVKLAADVRLKTDYKAS 486  
 Qy 309 EDVVPITGVVPDPETFATEKADGRMLQYMLKAGTPMDIPVYDVKVFIGSCTNSRRI 368  
 Db 416 GMNDDKUUPGKYYAVSTSNRNFEGROGPARTMLASPLTAANAITGVTTD -----P 466  
 Db 293 GMGIVSNKVNKNPLSLSI - EESNKVTKNKAALDGMFHGDLSLIGKQVNWVFLGSCNTGRIED 351  
 Qy 487 PHIAAOKSTVKPHDVERINQDAHEKDIADI1PEDNNGPHTNTSASVGTSAGLPKFTIL 546  
 Db 352 LROFAEFVKRKQKAANI - NALIVPSSKQVKERQATAGIDKYLAEAGFELREPGCSACLM 410  
 Qy 369 LRAAAAVVKGRKKAPVKSAMVPGSGLVKTQAEEGLDK1FEEAGFEWRAAGCSMCLG 428  
 Db 352 LROFAEFVKRKQKAANI - NALIVPSSKQVKERQATAGIDKYLAEAGFELREPGCSACLM 410  
 Qy 429 NPDLAPQECCASTSNRNPGRQGAGGRTHLSPVMAAGIVKLAADVRLKTDYKASPH 488  
 Db 411 NEDKVPKGECVSTSNRNPGRQGPARTLUVSPLTAALAVSGK1VDVREMLNXSSNNIQ 470  
 Qy 489 IAAVOKSTVKPHDVERINQDAHEKDIADI1PEDNNGPHTNTSASVGTSAGLPKFTILKG 548  
 Db 471 ISPIKR -----IXDEK -----TPRIMEKEFTIKS 494  
 Qy 549 IAAPLEKANYDFTDA1PKQFLKTKTGTGLGNALFYEMRNFEDGTEKSDFVLUKEPYRKAS 608  
 Db 495 TVVPLPITEDVDTDQIPARFLKATKPEGFKSLFCWRYNDGTPADFWN-NPLYSGQ 553  
 Qy 609 ILVCTGANPGGSSREHAPHALNDFGIRSVIAPSFDIFFNSFKGMLPIPIKD--QA 665  
 Db 554 ILV-AGKNFPGCSSREHAAWAIGDAGFVYVVSFFADIFRSNALNQNLIPQVSDAFLKS 612  
 Qy 666 QIEATAAEARAGKEFVLDLNPQLNQLKATGETICTFEEFKHLVNGLDDIGLTMQMED 725  
 Db 613 1FDVAVANAK - QELVVDLANQVISAGTDLKESPVINEYKKTCLLINGDDYDVISSIKD 670  
 Qy 726 KIAEPE 731  
 Db 671 KIEAYE 676  
 Qy 725 DKIAEFEA 732  
 Db 661 EAIAYEA 668  
 Qy 726 KIAEPE 731  
 Db 671 KIEAYE 676  
 RESULT 20  
 US-60-360-039-10463  
 ; Sequence 10463, Application US/60360039  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Chen, Xianfeng  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; TITTLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 ; FILE REFERENCE: 3B-10(52052)A  
 ; CURRENT APPLICATION NUMBER: US/60/360,039  
 ; CURRENT FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 10463  
 ; LENGTH: 676  
 ; TYPE: PRT  
 ; ORGANISM: Cytophaga hutchinsonii  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1). (676)  
 ; OTHER INFORMATION: unsure at all xaa locations  
 US-60-360-039-10463

Query Match 41.9%; Score 1697.5; DB 27; Length 676;  
 Best Local Similarity 48.5%; Pred. No. 6 6e-160; Mismatches 212; Indels 53; Gaps 10;  
 Macches 352; Conservative 109; Mismatches 212; Indels 53; Gaps 10;  
 TYPE: PRT  
 ORGANISM: *Bacillus thuringiensis*  
 US-60-360-039-1643

Query Match 41.5%; Score 1682.5; DB 27; Length 646;  
 Best Local Similarity 49.7%; Pred. No. 1.9e-158; Mismatches 196; Indels 81; Gaps 11;  
 Matches 359; Conservative 87; Mismatches 196; Indels 81; Gaps 11;

Qy 11 LYDKVYQAHVYDEKLDGTIVLVLIDRHLVHEVTSPOAFEGLNRAGKVRPDTLATTDHN 70  
 Db 5 LLDKWLWHRHVATNENGLDLTLVHLVHEVTSQPREGLRLTNRTVVRPDLTFATMDHN 64  
 Qy 71 VPTTSRKALKDIASTPKEDDSRTOCTVLEENVKERGTVYFGLSDKRGQVHVGEGQFT 130  
 Db 65 IPT-----KDWVN-TDRIAKQQLDTLRENCKQFVPLADIGDQEQVHVGELGLT 117  
 Qy 131 LPGTTVVGDSHTSPTGAFGALAFGIGTSEVHVLATQCLITKRSNMRQVGDGEALPGV 190  
 Db 175 GVTAKDVLVYIAQISAGGTGPFVETCGSAITSLSMEARTMTCNMS1EMGARGGM1APD 234

Qy 9 QTYLDKVYQAHVYDEKLDGTIVLVLIDRHLVHEVTSPOAFEGLNRAGKVRPDTLATTD 68  
 Db 1 KTLFEKWNWAVHVTTEVKDGPSPVYIDKOLINEVHTSPQAFAGTIGVFRPRTLATTD 60  
 Qy 69 HNPVPTTSRKALKDIASTPKEDDSRTOCTVLEENVKERGTVYFGLSDKRGQVHVGEGQFT 128  
 Db 61 HNPVPTKGONLP -----IVEDLSRFQVDKLTENCNKFGTVLTYLIGHASQGVHVGEGQFT 114  
 Qy 129 FTLPGTIVVCGDQHSTHGAAGALAFGIGTSEVHVLATQCLITKRSNMRQVGDGEALP 188  
 Db 115 TLLPGTIVVCGDQHSTHGAAGALAFGIGTSEVHVLATQCLITKRSNMRQVGDGEALP 174  
 Qy 189 GVSSKDVYVLAHAGTIGLPGAGTGTGAVIEFCGSVIRSLSMEARMSICNMS1EGGAGMVPD 248  
 Db 175 GVTAKDVLVYIAQISAGGTGPFVETCGSAITSLSMEARTMTCNMS1EMGARGGM1APD 234

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Db 1 RTUYQKHIDHTVCTLDQQ--GHVLLYIDTRQVANEYTSQQAFSGIREARTVNRPAATLA 58
QY 66 TUDHNVPTRTSRKALKDIAIFIKEEDSRQCVTLEENVKEFGVTYFGLSDRQGIVHVG 125
Db 59 VUDHVNPTR---APKRIATMPDAGGAR-QVSYFEECNDRFGIELFDVLDKRGEBHVAP 113
QY 126 EOGFTLQCTGTYVCGDSHTSTHGFAGFALRGIGTSSEVERNLATOLITKESKNMIIQDGE 185
Db 114 EOGFILPQMVVAAGDSHTTYGALGAFGRGIGSEIEHLILATQTLVYKRLKTLRVN 173
QY 186 LARGVSSCDVVLHAIIGITAGTGAIVIFCGSVIRSLSEARMSICNNSIEGGARAGMV 245
Db 174 LGAGVTSKDIIMALIEKIGASGATGYAIFTGPAISALSVEARMTICNNVAEARGAFM 233
QY 246 APPDEITEFVYLGRLAPKVDPSPEWKATQYQWKNLQSDPQAKYDIDVFDIADKDVIPTLWG 305
Db 234 ADDKVFLVQLHRRPAP--GKLUQDADHMKLHSDEGAVFREVILDAELEMWTG 291
QY 306 TSPEDEWVPTGUVVDPDETTAEKKADERTRMLOYNGLKGTMPDIPVVKVFGSCTNSR 365
Db 292 TSFDOQAAPKIAHVDPAAQDPDITRQGLRQALDYMGLTGPMLNEVTSHAFLQGSCMC 351
QY 366 IELRRAAAVWKGRKKAAVNKSAMWVPSQGLVKTQAEGLDKPFEAEPEWREBAGSMC 425
Db 352 IEDLIRDVVARVVRGKRVAAHVR-AMIVPGSTLVRNQADEGLAOIFLDACFEWROSGCWC 410
QY 426 LGNNDPDLAPQBERCASTSNRNFFGRQGAGGRTHLSPMVAAAGIVGKJADVRKLTDYKA 485
Db 411 LAMDDVLAQPGDCRCASSNRFGRQGAGARTHLMSPANVAA-ISGHTDVRTV--- 464
QY 486 SPHIAVYOKSTVTKPHVUDERINGDAHEKDIADIPIPEDDNNGPHTNTSASVGTTSAGLKPFTI 545
Db 465 -----ALFAXT-----MQPFDT 476
QY 546 LKGIAAPLEKANVDTAIIPKQFLKTIKRTGIGNALFYEMRNEDGTEKSDFVNUNKEPYR 605
Db 477 VSGSAAPFLASNIIDTVMPKQFLKGIDRQGLDRGLFFDLRFLASGEPRNPFEVUNQOW 536
QY 606 KASILVNTGANFGGSSRHEHAPWAINDFGIRSVIAPSEADIFFNSFKQGMLPIKQDA 665
Db 537 DAFLV-TGPNFQCGSSRHEAVWGLKQVGRALGTTFGIFVYNCQNRGVLQL-DA 594
QY 666 QI----EAIAAEARAGKEIIEVDIPLNQLNKATGTCIEVEEERKHCIVNGLDDIGTM 721
Db 595 QFKEVAEAIISVPA-T-RISVNLQQTBLELADG-TLIEFIDQLRKOSIILGLDAIGTL 651
QY 722 QMDKIAEFEAKMTRTBDGCGYLKKGQ 752
Db 652 ORTEOIRAFEARHLADNPWL--GXWQKNGR 679

RESULT 22
PCT-US02-03987-5730
; Sequence 5730, Application PC/TU0203987
; GENERAL INFORMATION:
; APPLICANT: Eltara Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELTRA-028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267, 636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 1811
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5730

```

OTHER INFORMATION: Xaa = Any Amino Acid  
PCT-US02-01987-5730

Query Match 41.1%; Score 1666.5; DB 1; Length 644;  
Best Local Similarity 48.7%; Prd. No. 7.e-157;  
Matches 352; Conservative 92; Mismatches 198; Gaps 10;

Qy 9 QTYLDKVLAHQHVDKEDDSRTQCVTLEENVKERGTVYFGLSDKRGIVHVGPEQ 128  
Db 3 QTLFDKVWNRHVLYKGKPEQVLYDHLVHEVTSQAFEGRLQNLKLRPLTEATLD 62

Qy 69 HNPVPTSRKALKDIASTKEDDSRTQCVTLEENVKERGTVYFGLSDKRGIVHVGPEQ 128  
Db 63 HNPVIT----DIFN-1KDEANKQTTLQKNAIDGVHIFDMSDEQGIVHMGVBPTG 115

Qy 129 FTLPGSTTVCGDSHTSTHGAFLAFAFGTSEVEHVLATOCLLTKRSKMRQIVDGEFLAP 188  
Db 116 LTQPGKTVCGDSHTATHGAFLAFAFGTSEVEHVLATOCLLTKRSKMRQIVDGEFLAP 175

Qy 189 QVSSKDVKVLHAIGIIGTAGGTGAVIEFGSVIRSLSMEARNSICNMSLEGGRAGMVPD 248  
Db 176 GYVAKDILHLIKTYGVDFGTGYALETGETKNSLMDGRMTCNMAEGAKYGIQPD 235

Qy 249 EITFEVYKGRPLAKYDSDPEWKAQKADGRMLQYQMLKAGTPMEDIYDVKWFIGCTNSRIED 368  
Db 236 DTFEYVKGRPPADNF----AKSVDKWRELYSDDDAI.FDRVIEFLDYLSTLEPQWTWGTNP 290

Qy 309 EDVVPITGVVVDPDPEFATEAKKADGRMLQYQMLKAGTPMEDIYDVKWFIGCTNSRIED 368  
Db 291 EMGVNNSEPFP----EISDINDQAYDNGCLEPGKQAKEDDLGIVFLGSCTNARLSD 343

Qy 369 IAAAAAVVKGRKKKAPVNSAMVPGSLVYKTOAEEGLKIFPEAGEPWRREAGCSMCLGM 428  
Db 344 LIEASHIVKGKVKHPNI-TATVPGSRTVKREAEKLQGDTTPKNAQFPEWREPCSCMCLGM 402

Qy 429 NPDILAQFQERCASTSNENFEGRQGAGRTHLNSPVMAAAGTIVGKLAQDVRKLTIDYKAPH 488  
Db 403 NPDQVPEGVHCASTSNENFEGRQGKARTHLNSPVMAAAGTIVGKLAQDVRKLTIDYKAPH 454

Qy 489 IAAQKSTVTKPHDVERINODAHEKDITADIPEPDNNGPHTNTSASVGTSGLPKFTILKG 548  
Db 455 -----  
Qy 549 IAAPLEKANVDTDAIIPKQFLKTIKRTGLNHALFYEMRNEFDTESKDFVNLKEPKRKS 608  
Db 470 KIVPLFDNDIITDQITIKVHKLRIKSGFGPPAFDEWRYLPDGSNDPENPKPQYKGS 529

Qy 609 ILVCTGANPGCSSREHAPWALNDFGRSVIAFDFIIFNNSFKNGMLPPIKFDQOIE 668  
Db 530 ILL-TGDNFEGCSSREHAAWALKDGFHIIAGSFDFYMNCTKNAMLPVILEKNA-E 587

Qy 669 AIAAEARAGKTEVDLPNQLKNTAGTGETCTFEVEEPRKHCLYNGLDDIGLTMQMEDKIA 728  
Db 588 HIAKYV---EIEVDLPNQTV--SSPDKSFFEIDETWKNLVNGLDDIAITLQYESLIE 641

Qy 729 EPE 731  
Db 642 EYE 644

RESULT 23  
US-09-815-242-5730  
GENERAL INFORMATION:  
/ APPLICANT: Haselbeck, Robert  
/ APPLICANT: Ohlsen, Kari L.  
/ APPLICANT: Zyskind, Judith W.  
/ APPLICANT: Wall, Daniel  
/ APPLICANT: Trawick, John D.  
/ APPLICANT: Carr, Grant J.  
/ APPLICANT: Yamamoto, Robert T.  
/ APPLICANT: Xu, H. Howard  
/ TITLE OF INVENTION: Identification of Essential Genes in

OTHER INFORMATION: Prokaryotes  
/ FILE REFERENCE: ELITRA.011A  
/ CURRENT APPLICATION NUMBER: US/09/815,242  
/ PRIOR APPLICATION NUMBER: 60/191,078  
/ PRIOR APPLICATION NUMBER: 60/200-03-21  
/ PRIOR APPLICATION NUMBER: 60/206,848  
/ PRIOR FILING DATE: 2000-05-23  
/ PRIOR FILING DATE: 2000-05-26  
/ NUMBER OF SEQ ID NOS: 14110  
/ SOFTWARE: FastSEQ for Windows Version 4.0  
/ SEQ ID NO: 5730  
/ LENGTH: 644  
/ TYPE: PRT  
/ ORGANISM: staphylococcus aureus  
/ FEATURE:  
/ NAME/KEY: VARIANT  
/ LOCATION: (1) .. (644)  
/ OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-815-242-5730

Query Match 41.1%; Score 1666.5; DB 22; Length 644;  
Best Local Similarity 48.7%; Prd. No. 7.e-157; Mismatches 198; Indels 81; Gaps 10;  
Matches 352; Conservative 92; Length 644;  
Qy 9 QTLYDKVLQAHVYDEKLDGTWLYLTDRLYHEVTSQAFEGRLNAGRKVRRPDCTLATTD 68  
Db 3 QTLFDKVWNRHVLYKGKPEQVLYDHLVHEVTSQAFEGRLQNLKLRPLTEATLD 62

Qy 69 HNPVPTSRKALKDIASTKEDDSRTQCVTLEENVKERGTVYFGLSDKRGIVHVGPEQ 128  
Db 63 HNPVIT----DIFN-1KDEANKQTTLQKNAIDGVHIFDMSDEQGIVHMGVBPTG 115

Qy 129 FTLPGSTTVCGDSHTSTHGAFLAFAFGTSEVEHVLATOCLLTKRSKMRQIVDGEFLAP 188  
Db 116 LTQPGKTVCGDSHTATHGAFLAFAFGTSEVEHVLATOCLLTKRSKMRQIVDGEFLAP 175

Qy 189 QVSSKDVKVLHAIGIIGTAGGTGAVIEFGSVIRSLSMEARNSICNMSLEGGRAGMVPD 248  
Db 176 GYVAKDILHLIKTYGVDFGTGYALETGETKNSLMDGRMTCNMAEGAKYGIQPD 235

Qy 249 EITFEVYKGRPLAKYDSDPEWKAQKADGRMLQYQMLKAGTPMEDIYDVKWFIGCTNSRIED 368  
Db 236 DTFEYVKGRPPADNF----AKSVDKWRELYSDDDAI.FDRVIEFLDYLSTLEPQWTWGTNP 290

Qy 309 EDVVPITGVVVDPDPEFATEAKKADGRMLQYQMLKAGTPMEDIYDVKWFIGCTNSRIED 368  
Db 291 EMGVNNSEPFP----EISDINDQAYDNGCLEPGKQAKEDDLGIVFLGSCTNARLSD 343

Qy 369 IAAAAAVVKGRKKKAPVNSAMVPGSLVYKTOAEEGLKIFPEAGEPWRREAGCSMCLGM 428  
Db 344 LIEASHIVKGKVKHPNI-TATVPGSRTVKREAEKLQGDTTPKNAQFPEWREPCSCMCLGM 402

Qy 429 NPDILAQFQERCASTSNENFEGRQGAGRTHLNSPVMAAAGTIVGKLAQDVRKLTIDYKAPH 488  
Db 403 NPDQVPEGVHCASTSNENFEGRQGKARTHLNSPVMAAAGTIVGKLAQDVRKLTIDYKAPH 454

Qy 489 IAAQKSTVTKPHDVERINODAHEKDITADIPEPDNNGPHTNTSASVGTSGLPKFTILKG 548  
Db 455 -----  
Qy 549 IAAPLEKANVDTDAIIPKQFLKTIKRTGLNHALFYEMRNEFDTESKDFVNLKEPKRKS 608  
Db 470 KIVPLFDNDIITDQITIKVHKLRIKSGFGPPAFDEWRYLPDGSNDPENPKPQYKGS 529

Qy 609 ILVCTGANPGCSSREHAPWALNDFGRSVIAFDFIIFNNSFKNGMLPPIKFDQOIE 668  
Db 530 ILL-TGDNFEGCSSREHAAWALKDGFHIIAGSFDFYMNCTKNAMLPVILEKNA-E 587

Qy 669 AIAAEARAGKTEVDLPNQLKNTAGTGETCTFEVEEPRKHCLYNGLDDIGLTMQMEDKIA 728  
Db 588 HIAKYV---EIEVDLPNQTV--SSPDKSFFEIDETWKNLVNGLDDIAITLQYESLIE 641

Qy 729 EPE 731  
Db 642 EYE 644

RESULT 23  
US-09-815-242-5730  
GENERAL INFORMATION:  
/ APPLICANT: Haselbeck, Robert  
/ APPLICANT: Ohlsen, Kari L.  
/ APPLICANT: Zyskind, Judith W.  
/ APPLICANT: Wall, Daniel  
/ APPLICANT: Trawick, John D.  
/ APPLICANT: Carr, Grant J.  
/ APPLICANT: Yamamoto, Robert T.  
/ APPLICANT: Xu, H. Howard  
/ TITLE OF INVENTION: Identification of Essential Genes in

Query Match 41.1%; Score 1666.5; DB 22; Length 644;  
Best Local Similarity 48.7%; Prd. No. 7.e-157; Mismatches 198; Indels 81; Gaps 10;  
Matches 352; Conservative 92; Length 644;  
Qy 9 QTLYDKVLQAHVYDEKLDGTWLYLTDRLYHEVTSQAFEGRLNAGRKVRRPDCTLATTD 68  
Db 3 QTLFDKVWNRHVLYKGKPEQVLYDHLVHEVTSQAFEGRLQNLKLRPLTEATLD 62

Qy 69 HNPVPTSRKALKDIASTKEDDSRTQCVTLEENVKERGTVYFGLSDKRGIVHVGPEQ 128  
Db 63 HNPVIT----DIFN-1KDEANKQTTLQKNAIDGVHIFDMSDEQGIVHMGVBPTG 115

Qy 129 FTLPGSTTVCGDSHTSTHGAFLAFAFGTSEVEHVLATOCLLTKRSKMRQIVDGEFLAP 188  
Db 116 LTQPGKTVCGDSHTATHGAFLAFAFGTSEVEHVLATOCLLTKRSKMRQIVDGEFLAP 175

Qy 189 QVSSKDVKVLHAIGIIGTAGGTGAVIEFGSVIRSLSMEARNSICNMSLEGGRAGMVPD 248  
Db 176 GYVAKDILHLIKTYGVDFGTGYALETGETKNSLMDGRMTCNMAEGAKYGIQPD 235

Qy 249 EITFEVYKGRPLAKYDSDPEWKAQKADGRMLQYQMLKAGTPMEDIYDVKWFIGCTNSRIED 368  
Db 236 DTFEYVKGRPPADNF----AKSVDKWRELYSDDDAI.FDRVIEFLDYLSTLEPQWTWGTNP 290

Qy 309 EDVVPITGVVVDPDPEFATEAKKADGRMLQYQMLKAGTPMEDIYDVKWFIGCTNSRIED 368  
Db 291 EMGVNNSEPFP----EISDINDQAYDNGCLEPGKQAKEDDLGIVFLGSCTNARLSD 343

Qy 369 IAAAAAVVKGRKKKAPVNSAMVPGSLVYKTOAEEGLKIFPEAGEPWRREAGCSMCLGM 428  
Db 344 LIEASHIVKGKVKHPNI-TATVPGSRTVKREAEKLQGDTTPKNAQFPEWREPCSCMCLGM 402

Qy 429 NPDILAQFQERCASTSNENFEGRQGAGRTHLNSPVMAAAGTIVGKLAQDVRKLTIDYKAPH 488  
Db 403 NPDQVPEGVHCASTSNENFEGRQGKARTHLNSPVMAAAGTIVGKLAQDVRKLTIDYKAPH 454

Qy 489 IAAQKSTVTKPHDVERINODAHEKDITADIPEPDNNGPHTNTSASVGTSGLPKFTILKG 548  
Db 455 -----  
Qy 549 IAAPEKANVDTDAIIPKQFLKTIKRTGLNHALFYEMRNEFDTESKDFVNLKEPKRKS 608  
Db 588 HIAKYV---EIEVDLPNQTV--SSPDKSFFEIDETWKNLVNGLDDIAITLQYESLIE 641

Qy 729 EPE 731  
Db 642 EYE 644

RESULT 23  
US-09-815-242-5730  
GENERAL INFORMATION:  
/ APPLICANT: Haselbeck, Robert  
/ APPLICANT: Ohlsen, Kari L.  
/ APPLICANT: Zyskind, Judith W.  
/ APPLICANT: Wall, Daniel  
/ APPLICANT: Trawick, John D.  
/ APPLICANT: Carr, Grant J.  
/ APPLICANT: Yamamoto, Robert T.  
/ APPLICANT: Xu, H. Howard  
/ TITLE OF INVENTION: Identification of Essential Genes in

QY 609 ILVCTGANFGCSSREHAPWALNDFGIPTSVIAPSFAFDIPFNNSPKNGMLPPIKDQACIE 668  
 Db 530 ILL-TGDNFGCGSSREHAWALKDYGFGHIIAGSFSDIFYMCNTKNAULPYLEKNAR-E 587  
 QY 669 AIAEARGKEIEVDLNLQNLKATGETCTCPEVERFRKHLVINGLDDIGLTMQMEDKIA 728  
 Db 588 HLAKYV---EIEVLPNQTV---SSPDKSFPHEFIDETWKNKLUVNGLDDIAITQYESLIE 641  
 QY 729 EFE 731  
 Db 642 KYE 644

RESULT 24  
 US-10-072-851-5730  
 ; Sequence 5730, Application US/10072851  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carr, Grant J.  
 ; APPLICANT: Xu, H. Howard  
 ; APPLICANT: Foulkes, J. Gordon  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Hasebeck, Robert  
 ; APPLICANT: Ohlsen, Kari L.  
 ; APPLICANT: Zyskind, Judith W.  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John D.  
 ; APPLICANT: Yamamoto, Robert T.  
 ; APPLICANT: Roemer, Terry  
 ; APPLICANT: Jiang, Bo  
 ; APPLICANT: Boone, Charles  
 ; APPLICANT: Bussey, Howard  
 ; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C  
 ; TITLE OF INVENTION: Proliferation  
 ; FILE REFERENCE: ELTRA 028A  
 ; CURRENT APPLICATION NUMBER: US/10/072,851  
 ; CURRENT FILING DATE: 2002-07-08  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 15811  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 5730  
 ; LENGTH: 644  
 ; TYPE: PRT  
 ; ORGANISM: *Staphylococcus aureus*  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: (1)..(644)  
 ; OTHER INFORMATION: Xaa = Any Amino Acid  
 ; US-10-072-851-5730

Query Match 41.1%; Score 1666.5; DB 24; Length 644;  
 Best Local Similarity 48.7%; Pred. No. 7.8e-157; Mismatches 92; Nucleotides 198; Indels 81; Gaps 10; Matches 352; Conservative 92; Mismatches 198; Indels 81; Gaps 10; Seq ID No 1009

QY 9 QTLQYKVLQAHVYDEKLDGTIVLVLIDRHLVHEVTSPOAFEGLNRAGKVRPDTLTD 68  
 Db 3 QTLFDKWRNHRVLYKGKLGEPOLQYIIDLHLHEVTSPOAFEGLNLQRKURRPDTLTD 62

QY 6 9 HNVPTTSRKALKDIASFIKEDSRTQCVTLEENVKERFGVTVFGLSDKRGQGVIVVGPQG 128  
 Db 6 3 HNVPTI----DIFN-IKDEIAKQOITLQRNAIDFGVHIFMGSDPQGIVVNGPETG 115

QY 129 FTLPGTIVVCGDSHTSTGAGFAGLAFGGTSEVERHVLATCQLTKRSKMRDVGELAP 188  
 Db 116 LTQPGKTRIVCGDSHTATGAGFAGLAFGGTSEVERHVLATCQLTKRSKMRDVGELAP 175

QY 189 GVSSKQDVLTHAIGIIGTAGGTCAVIEFGSVTRSLSMARMSTCNMSTEGARAGMVPD 248  
 Db 176 GYVAKOILILHLKTYGVFGTGYALEFGETKLNLSMDGRMTINMAIEGGAKYGIQD 235

QY 249 EITFEVKGRLPLAKVPSPEWHKATQWKNLQSDPGAXXIDVFDIAKDVIPILTWGSP 308

QY 609 ILVCTGANFGCSSREHAPWALNDFGIPTSVIAPSFAFDIPFNNSPKNGMLPPIKDQACIE 668  
 Db 530 ILL-TGDNFGCGSSREHAWALKDYGFGHIIAGSFSDIFYMCNTKNAULPYLEKNAR-E 587  
 QY 369 LRAAAAVVKGKAKPNUKVSAMNPSPGSGLVQKVOAEEGDKPFEAEPEWREAGCSCMCLGM 428  
 Db 344 LIEASHIVKGKVKHENI-TAIIVPGSRTVKRREAKLUGIDTIFRNAGPEWREPGCSCMCLGM 402

QY 429 NPDILAPQERCCASTSNRNPFGRQGGRTHMSPWAAGAGVKGKLAQYKTDYKASPH 488  
 Db 403 NPDQVPEGVHCASTSNRNPFGRQGKARTHLVSPPAAMAAA1HGFVVDVRYV-..... 454

QY 489 IAYQKSTVTPKPHVDERINQDAHEKDIADIPEPDNNPHTNTSASYGTSAGFVKFTILKG 548  
 Db 455 -----.....-VXMAAIKPKITYKG 469

QY 549 IAAPEAKANVDTDAPKOFKTRKTRKGFLGNAFLFYMRFNBDGTEKSDFVNLKREPKAS 608  
 Db 470 KIVPLFENDNIDTDQITPKVHLKRSKSGFGPFAFDWRYLPDGSNDPFPNPKPQYKGS 529

QY 609 ILVCTGANFGCSSREHAPWALNDFGCIRSVIAPSFAFDIPFNNSPKNGMLPPIKDQACIE 668  
 Db 530 ILL-TGDNFGCGSSREHAWALKDYGFGHIIAGSFSDIFYMCNTKNAULPYLEKNAR-E 587  
 QY 669 AIAEARGKEIEVDLNLQNLKATGETCTCPEVERFRKHLVINGLDDIGLTMQMEDKIA 728  
 Db 588 HLAKYV---EIEVLPNQTV---SSPDKSFPHEFIDETWKNKLUVNGLDDIAITQYESLIE 641

QY 729 EFE 731  
 Db 642 KYE 644

RESULT 25  
 US-60-242-578-1009  
 ; Sequence 1009, Application US/60242578  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hasebeck, R  
 ; APPLICANT: Ohlsen, K.  
 ; APPLICANT: Zyskind, J. W.  
 ; TITLE OF INVENTION: Genes Identified as essential in  
 ; TITLE OF INVENTION: *Staphylococcus aureus*  
 ; FILE REFERENCE: ELTRA.01PR2  
 ; CURRENT APPLICATION NUMBER: US/60/242,578  
 ; CURRENT FILING DATE: 2000-10-23  
 ; NUMBER OF SEQ ID NOS: 1057  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 1009  
 ; LENGTH: 644  
 ; TYPE: PRT  
 ; ORGANISM: *Staphylococcus aureus*  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: (1)..(644)  
 ; OTHER INFORMATION: Xaa = Any Amino Acid  
 ; US-60-242-578-1009

Query Match 41.1%; Score 1666.5; DB 27; Length 644;  
 Best Local Similarity 48.7%; Pred. No. 7.8e-157; Mismatches 92; Nucleotides 198; Indels 81; Gaps 10; Matches 352; Conservative 92; Mismatches 198; Indels 81; Gaps 10; Seq ID No 1009

QY 9 QTLQYKVLQAHVYDEKLDGTIVLVLIDRHLVHEVTSPOAFEGLNRAGKVRPDTLTD 68  
 Db 3 QTLFDKWRNHRVLYKGKLGEPOLQYIIDLHLHEVTSPOAFEGLNLQRKURRPDTLTD 62

QY 6 9 HNVPTTSRKALKDIASFIKEDSRTQCVTLEENVKERFGVTVFGLSDKRGQGVIVVGPQG 128  
 Db 6 3 HNVPTI----DIFN-IKDEIAKQOITLQRNAIDFGVHIFMGSDPQGIVVNGPETG 115

QY 129 FTLPGTIVVCGDSHTSTGAGFAGLAFGGTSEVERHVLATCQLTKRSKMRDVGELAP 188  
 Db 116 LTQPGKTRIVCGDSHTATGAGFAGLAFGGTSEVERHVLATCQLTKRSKMRDVGELAP 175

QY 69 HNVPTTSRKALKDIASFIKEDSRTQCVTLEENVKERFGVTVFGLSDKRGQGVIVVGPQG 128  
 Db 63 HNVPTI----DIFN-IKDEIAKQOITLQRNAIDFGVHIFMGSDPQGIVVNGPETG 115

QY 129 FTLPGTIVVCGDSHTSTGAGFAGLAFGGTSEVERHVLATCQLTKRSKMRDVGELAP 188

116	LTPGKTIYVGDSHTATHAIFGFAAAGTGTSEVEVPAQTLWQTPKPNLKIDINGTLPT	175
189	GVSSKDVYLHAIGIITGAGCTGAVIEFCGSVIRSLMSARMSICNMSIEGGARAGMVAPD	248
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
176	GIVADITLHLIKIYGVDFGTGAYLEFTGETIKNLSMDGRNTICMAIEGAKYGIQPD	235
Ddb		
249	BTTPYEYLGRPLAKYKDSPEWHKATQYKWLQSDGAKYDIDVFDKDIVPTLWGTSTP	308
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
236	DTTPEYVKGRRPFDNFV----AKSVDFKWRRELYSDDAIFRVRIVEDVSTLSEPOVWTGNT	290
Ddb		
309	EDVVPVTPGVVPDPETFATEAKKADGRMRLOYMGKLAGTPMEDIIPYDKVFLGSCTNRIED	368
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
291	EMGTFNFSFPP----EISDINDORAYDMGLFGQKAEDIDGYVFLGSCTNARLSD	343
Ddb		
369	LRAAAVVKGRKKAPEVKVNSAMVPPGSLYRKTQAEBGLDKIIFEEAGFENWEAGCSNCLGM	428
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
344	LIEASHIVKGKNTVHENI-TAIVVPGSRTVKREAEKLGDLTIFKNAFGEWRPEPGCSMCLGM	402
Ddb		
429	NPDTLAPQRCRCASTNRNPFEGROGGRGRTLMSPVMAAAAGIVGKLADEVLTDXKASPH	488
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
403	NPDQFPEGVHCASTSNRNFGRQGGARTHLPVSPAAAIAHGFVDFVRKV-----	454
Ddb		
489	IAAYQKSTVTKPHYDERINODAHEKDIADIPEPDNNGPHNTTSASVGTSAAGLPKFTILKG	548
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
455	-----VVXMAIKPTTYKG-----VVXMAIKPTTYKG	469
Ddb		
549	IAAPLEKANVDTDAIIPKOPBLKTKRTGLGNALFYEMRFNEDGTKEKSDFVNLKEPYRKAS	608
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
470	KIVPLFNDNIDDTQDQIPKVHLKRITSKSGFPPAFDWRYLPDGSNPDENPKQPKQGAS	529
Ddb		
609	ILVCTGANFRCGSSEHAPWALDGTIRSYIAPSFDIFFNSFNGMLPPIRKQDQF	668
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
530	ILI-TGDNFGCGSSSEHAAWALDKYGFHIIAGSSDFIMNCTKANMLPVLEKNAR-E	587
Ddb		
669	AIAAEARAKGKETEVDLPNOLIJKNATGETICTFEEFRKHICLNGDDIGITMOWEDKIA	728
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
588	HLAKYV---EIEVDLPEQNTV---SSPDKSFPHEIIDETWKNKLVNGDDIAITLQYESLIE	641
Ddb		
729	EEF 731	
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :    :	
642	KYE 644	
Ddb		

Search completed: March 17, 2003, 08:53:54  
Job time : 169 secs